

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: Nikolaus (Klaus) Theres  
 (B) STREET: Schiffgesweg 30  
 (C) CITY: Pulheim  
 (D) STATE: NRW  
 (E) COUNTRY: Germany  
 (F) POSTAL CODE: 50259  
 (G) TELEPHONE: + 49 2234 89386

(ii) TITLE OF INVENTION: PLANTS WITH CONTROLLED SIDE-SHOOT FORMATION  
 AND/OR ABSCISSION ZONE FORMATION

(iii) NUMBER OF SEQUENCES: 14

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1729 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCTCTGTCCT TCCCCCAGG TCCCCTTTTT TTCCTTTCTC TCTCTCCTTT ATTTCTCTTT	60
TCATAAGCAT ATTCTTTCTC TCTCTAGGGT TTTCACTTTC ACCTGAAATA GTGTTGTTAA	120
ATTGAATGAT ATGTTAGGAT CCTTTGGTTC TTCATCATCT CAATCTCACC CTCATCATGA	180
TGAAGAATCT TCTGATCATC ATCAACAGCG TAGATTCAACC GCTACTGCTA CAACTATCAC	240
CACCACCACC ATCACTACCT CACCAGCTAT TCAAATCCGC CAGCTACTCA TTAGCTGTGC	300
GGAGTTGATT TCGCAGTCCG ATTTCTCGGC CGCGAAAAGA CTCCTTACTA TATTATCAAC	360
TAACTCATCT CCTTTTGGTG ATTCAACTGA ACGGTTAGTC CATCAATTTA CTCGCGCACT	420
TTCCCTTCGT CTCAACCGCT ATATATCGTC AACCACCAAT CATTTTCATGA CACCTGTTGA	480
AACAACTCCA ACTGATTCTT CTTCTTCGTC ATCATTAGCT CTAATTCAAT CATCATATCT	540
ATCTCTAAAC CAAGTTACCC CTTTCATAAG GTTTACTCAA TTAACCGCTA ATCAAGCGAT	600

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TTTAGAAGCG ATTAACGGTA ATCATCAAGC AATCCACATC GTTGATTTTCG ACATTAATCA 660  
 CGGGGTTCAA TGGCCACCGT TAATGCAAGC ACTAGCTGAT CGTTACCCTG CTCCCCTCT 720  
 TCGAATCACC GGTACTGGAA ATGACCTTGA TACCCTTCGT AGAACAGGTG ATCGTTTAGC 780  
 TAAATTTGCT CACTCATTAG GGTTGAGATT TCAATTCCAT CCTCTTTATA TAGCCAATAA 840  
 TAACCACGAT CACGATGAAG ATCCTTCTAT TATTTCTCTC ATTGTACTAC TCCCTGATGA 900  
 AACCTAGCT ATCAACTGTG TTTTCTACCT CCACCGCCTT TTAAGAGACC GCGAAAAGTT 960  
 AAGGATTTTT TTGCATAGGG TTAAGTCAAT GAACCCTAAA ATTGTTACAA TCGCGGAGAA 1020  
 GGAAGCAAAT CATAACCATC CTCTTTTTTT ACAAGATTC ATCGAGGCGT TGGATTATTA 1080  
 TACAGCTGTG TTTGATTAC TGGAAGCTAC ATTGCCACCG GGTAGTCGAG AGAGGATGAC 1140  
 AGTTGAACAA GTGTGGTTTG GGAGAGAGAT TGTTGATATC GTTGCGATGG AAGGAGATAA 1200  
 AAGGAAAGAA AGACATGAAA GGTTTAGATC ATGGGAAGTT ATGTTGAGGA GTTGTGGATT 1260  
 TAGTAATGTT GCTTTAAGCC CTTTTCGATT ATCACAAGCT AAGCTTCTTT TGAGACTTCA 1320  
 TTATCCTTCT GAAGGCTATC AACTCGGAGT TTCGAGTAAT TCTTCTTCT TAGGTTGGCA 1380  
 AAATCAACCC CTTTTCTCCA TCTCGTCTTG GCGTTGAGAA AAATATCAA ATAGCCAAC 1440  
 TCAGAGGGTA ATTAAGACTA CTGATAGTTT AGGAGGGATC TGAAGAAAAC GCGTGGAGTG 1500  
 AAAACCTAA ATAACCAGAT TTTCTAATGA AGTTGTAGTA GTAGAAATTT GCATGGTGAA 1560  
 GAACAATATT GAAGAGGTAT TGAAATTTCA TGTTTTTTTT GTTTTACTTA TTGATATGAA 1620  
 TGTTTTAAAA TTTTAAACAT AGAGGACTAG GTTGATGATA TATAGTATTT AAGTTAACTA 1680  
 GTCTTTGTAT AACGCAAGAT CTTGATCAAC TTATTTTAT TTTAATTA 1729

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Gly Ser Phe Gly Ser Ser Ser Ser Gln Ser His Pro His His  
 1 5 10 15  
 Asp Glu Glu Ser Ser Asp His His Gln Gln Arg Arg Phe Thr Ala Thr  
 20 25 30  
 Ala Thr Thr Ile Thr Thr Thr Thr Ile Thr Thr Ser Pro Ala Ile Gln  
 35 40 45  
 Ile Arg Gln Leu Leu Ile Ser Cys Ala Glu Leu Ile Ser Gln Ser Asp  
 50 55 60

Phe Ser Ala Ala Lys Arg Leu Leu Thr Ile Leu Ser Thr Asn Ser Ser  
 65 70 75 80  
 Pro Phe Gly Asp Ser Thr Glu Arg Leu Val His Gln Phe Thr Arg Ala  
 85 90 95  
 Leu Ser Leu Arg Leu Asn Arg Tyr Ile Ser Ser Thr Thr Asn His Phe  
 100 105 110  
 Met Thr Pro Val Glu Thr Thr Pro Thr Asp Ser Ser Ser Ser Ser  
 115 120 125  
 Leu Ala Leu Ile Gln Ser Ser Tyr Leu Ser Leu Asn Gln Val Thr Pro  
 130 135 140  
 Phe Ile Arg Phe Thr Gln Leu Thr Ala Asn Gln Ala Ile Leu Glu Ala  
 145 150 155 160  
 Ile Asn Gly Asn His Gln Ala Ile His Ile Val Asp Phe Asp Ile Asn  
 165 170 175  
 His Gly Val Gln Trp Pro Pro Leu Met Gln Ala Leu Ala Asp Arg Tyr  
 180 185 190  
 Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly Asn Asp Leu Asp Thr  
 195 200 205  
 Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Phe Ala His Ser Leu Gly  
 210 215 220  
 Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala Asn Asn Asn His Asp  
 225 230 235 240  
 His Asp Glu Asp Pro Ser Ile Ile Ser Ser Ile Val Leu Leu Pro Asp  
 245 250 255  
 Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu His Arg Leu Leu Lys  
 260 265 270  
 Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg Val Lys Ser Met Asn  
 275 280 285  
 Pro Lys Ile Val Thr Ile Ala Glu Lys Glu Ala Asn His Asn His Pro  
 290 295 300  
 Leu Phe Leu Gln Arg Phe Ile Glu Ala Leu Asp Tyr Tyr Thr Ala Val  
 305 310 315 320  
 Phe Asp Ser Leu Glu Ala Thr Leu Pro Pro Gly Ser Arg Glu Arg Met  
 325 330 335  
 Thr Val Glu Gln Val Trp Phe Gly Arg Glu Ile Val Asp Ile Val Ala  
 340 345 350  
 Met Glu Gly Asp Lys Arg Lys Glu Arg His Glu Arg Phe Arg Ser Trp  
 355 360 365  
 Glu Val Met Leu Arg Ser Cys Gly Phe Ser Asn Val Ala Leu Ser Pro  
 370 375 380  
 Phe Ala Leu Ser Gln Ala Lys Leu Leu Leu Arg Leu His Tyr Pro Ser  
 385 390 395 400

Gln Asn Gln Pro Leu Phe Ser Ile Ser Ser Trp Arg  
420 425

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(iii) HYPOTHETIC: NO

TTAGGGTTTT CACTCCACGC

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(iii) HYPOTHETIC: NO

TCCCCTTTTT TTCCTTTCTC TC

22

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(iii) HYPOTHETIC: NO

TTTCCCACTC AAGCCAATC

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20

22

19

60

120

ACAACGACCT CACCAGCTAT TCAAATCCGC CAGCTACTCA TTAGCTGTGC GGAGTTGATT 180  
 TCGCGGTCCG ATTTCTCGGC CGCGAAAAGA CTCCTTACCA TATTATCAAC TAACTCTTCT 240  
 CCTTTTGGTG ATTCAACTGA ACGGTTAGTC CATCAGTTTA CTCGCGCACT TTCCCTTCGT 300  
 CTCAACCGCT ATATATCGTC AACCACCAAT CATTTCATGA CACCTGTTGA AACAACTCCA 360  
 ACTGATTCTT CATCTTCGTT GCCATCGTCA TCATTAGCTC TAATTCAATC ATCATATCAT 420  
 TCTCTAAATC AAGTTACCCC TTTTATAAGG TTTACTCAAT TAACCGCTAA TCAAGCGATT 480  
 TTAGAAGCGA TTAACGGTAA TCATCAAGCA ATCCACATCG TTGATTTCGA CATTAAATCAC 540  
 GGGGTTCAAT GGCCACCGTT AATGCAAGCA CTAGCTGATC GTTACCCTGC TCCTACTCTT 600  
 CGAATCACCG GTACTGGAAA TGACCTTGAT ACCCTTCGTA GAACAGGTGA TCGTTTAGCT 660  
 AAATTTGCTC ACTCATTAGG GTTGAGATTT CAATTCCATC CTCTTTATAT CGCCAATAAT 720  
 AACCGCGATC ACGGTGAAGA TCCTTCTATT ATTTCTCCA TTGTACTTCT CCCTGATGAA 780  
 ACCCTAGCTA TCAACTGTGT TTTCTATCTC CACCGCCTTT TAAAAGACCG CGAAAAATTA 840  
 AGGATTTTTT TGCATAGGGT TAAGTCAATG AACCCTAAAA TTGTTACAAT CGCGGAGAAG 900  
 GAAGCAAATC ATAACCATCC TCTTTTTTTA CAAAGATTTA TCGAGGCGTT GGATTATTAT 960  
 ACAGCTGTGT TTGATTCATT GGAAGCTACA TTGCCACCGG GTAGTCGTGA GAGGATGACA 1020  
 GTTGAACAAG TGTGGTTTGG GAGAGAAATT GTTGATATCG TGGCGATGGA AGGAGATAAA 1080  
 AGGAAAGAAA GACATGAAAG GTTTAGATCA TGGGAAGTTA TGTTGAGGAG TTGTGGATTT 1140  
 AGTAATGTTG CTTTAAGCCC TTTTGCATTA TCACAAGCTA AGCTTCTTTT GAGACTACAT 1200  
 TATCCTTCTG AAGGCTATCA ACTCGGAGTT TCGAGTAATT CTTTCTTCTT AGGTTGGCAA 1260  
 AATCAACCTC TTTTCTCCAT CTCGTCTTGG CGTTGA 1296

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Solanum tuberosum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Leu Gly Ser Phe Gly Ser Ser Ser Ser Gln Ser His Pro His His  
 1 5 10 15  
 Asp Glu Glu Ser Ser Asp His His Gln Arg Arg Arg Phe Thr Ala Thr  
 20 25 30  
 Thr Thr Thr Ile Thr Thr Thr Thr Thr Thr Thr Ser Pro Ala Ile Gln  
 35 40 45



Tyr	Pro	Ser	Glu	Gly 405	Tyr	Gln	Leu	Gly	Val 410	Ser	Ser	Asn	Ser	Phe 415	Phe
Leu	Gly	Trp	Gln 420	Asn	Gln	Pro	Leu	Phe 425	Ser	Ile	Ser	Ser	Trp 430	Arg	

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 Base pairs
  - (B) TYPE: Nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
- (iii) HYPOTHETIC: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CARTGGCCNC CNYTNATGCA

20

(2) INFORMATION FOR SEQ ID NO: 12:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 Base pairs
      (B) TYPE: Nucleotide
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:   synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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TGRTTYTGCC ANCCNARRAA

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(2) INFORMATION FOR SEQ ID NO: 13:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 687 Base pairs
      (B) TYPE: Nucleotide
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Arabidopsis thaliana

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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GAGAGGTCAT	CAAACCCTAG	CAGTCCACCT	CCATCTCTCC	GCATAACCGG	ATGCGGTCGA	60
GATGTAACCG	GATTAAACCG	AACTGGAGAC	CGGTTAACCC	GGTTCGCTGA	CTCTTTAGGT	120
CTCCAATTCC	AGTTTCACAC	GCTAGTGATC	GTAGAAGAAG	ATCTCGCCGG	ACTTTTGCTA	180



CAGATCCGAT TGTTAGCTCT CTCAGCCGTA CAAGGAGAGA CCATTGCCGT CAATTGTGTT 240  
 CACTTCCTCC AAAAAATATT TAACGACGAT GGAGATATGA TCGGTCACTT CTTGTCAGCG 300  
 ATCAAGAGCT TAAACTCTAG AATCGTTACA ATGGCAGAGA GAGAAGCTAA TCATGGAGAT 360  
 CACTCGTTCT TGAATAGATT CTCTGAGGCA GTGGATCATT ACATGGCGAT CTTTGATTCTG 420  
 TTGGAAGCGA CGTTGCCGCC AAATAGCCGA GAGAGACTAA CCCTAGAGCA ACGGTGGTTC 480  
 GGTAAGGAGA TTTTGGATGT TGTGGCGGCG GAAGAGACGG AGAGAAAGCA AAGACATCGG 540  
 AGGTTTGAGA TTTGGGAAGA GATGATGAAG AGGTTTGGTT TCGTTAACGT TCCTATTGGA 600  
 AGCTTTGCTT TGTCTCAAGC TAAGCTTCTT CTTAGACTTC ATTATCCTTC AGAAGGTTAT 660  
 AATCTTCAGT TCCTTAACAA TTCTTTG 687

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Glu	Arg	Ser	Ser	Asn	Pro	Ser	Ser	Pro	Pro	Pro	Ser	Leu	Arg	Ile	Thr	1	5	10	15
Gly	Cys	Gly	Arg	Asp	Val	Thr	Gly	Leu	Asn	Arg	Thr	Gly	Asp	Arg	Leu	20	25	30	
Thr	Arg	Phe	Ala	Asp	Ser	Leu	Gly	Leu	Gln	Phe	Gln	Phe	His	Thr	Leu	35	40	45	
Val	Ile	Val	Glu	Glu	Asp	Leu	Ala	Gly	Leu	Leu	Leu	Gln	Ile	Arg	Leu	50	55	60	
Leu	Ala	Leu	Ser	Ala	Val	Gln	Gly	Glu	Thr	Ile	Ala	Val	Asn	Cys	Val	65	70	75	80
His	Phe	Leu	His	Lys	Ile	Phe	Asn	Asp	Asp	Gly	Asp	Met	Ile	Gly	His	85	90	95	
Phe	Leu	Ser	Ala	Ile	Lys	Ser	Leu	Asn	Ser	Arg	Ile	Val	Thr	Met	Ala	100	105	110	
Glu	Arg	Glu	Ala	Asn	His	Gly	Asp	His	Ser	Phe	Leu	Asn	Arg	Phe	Ser	115	120	125	
Glu	Ala	Val	Asp	His	Tyr	Met	Ala	Ile	Phe	Asp	Ser	Leu	Glu	Ala	Thr	130	135	140	
Leu	Pro	Pro	Asn	Ser	Arg	Glu	Arg	Leu	Thr	Leu	Glu	Gln	Arg	Trp	Phe	145	150	155	160

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Gly	Lys	Glu	Ile	Leu	Asp	Val	Val	Ala	Ala	Glu	Glu	Thr	Glu	Arg	Lys
				165					170					175	
Gln	Arg	His	Arg	Arg	Phe	Glu	Ile	Trp	Glu	Glu	Met	Met	Lys	Arg	Phe
			180					185					190		
Gly	Phe	Val	Asn	Val	Pro	Ile	Gly	Ser	Phe	Ala	Leu	Ser	Gln	Ala	Lys
		195					200					205			
Leu	Leu	Leu	Arg	Leu	His	Tyr	Pro	Ser	Glu	Gly	Tyr	Asn	Leu	Gln	Phe
	210					215					220				
Leu	Asn	Asn	Ser	Leu											
225															

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